

FIGURE 78

CTCCTCCAGGTTGCCAGCGCCAGAAATGCGGCTTCTGGTCTGCTATGGGGTTGCCTGCTGCT
 CCCAGGTTATGAAGCCCTGGAGGGCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGT
 CCTGTCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGT
 GGGATCTCTTCTCTCGTCTCTGGCCACCATCTATGCAGAGAAGAAGGCCAGGAGACAAAT
 GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTGTGACCCCTGTGGA
 ACCTCACCCCTGCAAGACGCTGGGGAGTACTGGTGTGGGCTCGAAAAACGGGGCCCCGATGAG
 TCTTTACTGATCTCTCTGTTCGTCTTTCCAGGACCTGCTGTCTCCCTCCCTTCTCCCAC
 CTTCAGCCTCTGGCTACAACACGCCTGACGCCCAAGGCAAAAGCTCAGCAAAACCCAGCCCC
 CAGGATTGACTTCTCTGGGCTTACCCGGCAGCCACCAAGCCAAAGCAGGGGAGACAGGG
 GCTGAGGCCCCCTCCATTGCCAGGGACTTCCAGTACGGGCACGAAAGGACTTCTCAGTACAC
 AGGAACCTCTCTCACCCAGCGACCTCTCTCTGACGGGAGCTCCCCCCCCCATGCGAGC
 TGGACTCCACCTCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCCAGG
 GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCCCTGGTGTCTGTGAGCCCTTCTGTGAGC
 CGCAGGCCCTGATCGCCTTCTGACGCCACCTGCTCTCTGTGAGAAAGGAAGCTCAACAGGCCA
 CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCAGCCTTGACTGCGGAGGAAAAGGAAGCC
 CTTTCCAGGCCCTGAGGGGGACGTGATCTCGATGCCTCCCTCCACATCTGAGGAGGA
 GCTGGGCTTCTCGAAGTTTGTCTCAGCGTAGGGCAGGAGGCCCTCTGGCCAGGCCAGCAGT
 GAAGCAGTATGGCTGGCTGGATCAGCACCGATTCCCGAAAGCTTTCCACCTCAGCCTCAGAG
 TCCAGCTGCCCGGACTCAGGGCTTCCCCACCTCCCCAGGCTCTCCTCTTGATGTTTCCA
 GCCTGACCTAGAAGCGTTTGTGACGCCCTGGAGCCAGAGCGGTGGCTTGTCTTCCGGCTG
 GAGACTGGGACATCCCTGATAGGTTACATCCCTGGGCAGAGTACCAGGCTGTGACCCCTCA
 CAGGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACTCTTGGGC
 CTCATGCCCAGTGTGCGACCCCTGCCCTTCTCCCACTCCAGACCCACCTTGTCTTCCCTCCC
 TGGCGTCTCTCAGACTTAGTCCCACGGTCTCTGTCATCAGCTGGTGTGAGAGGAGCATGCT
 GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACTGCATCCAGCCCTTCAGGAAGCCCT
 GTGAAAAACGTGATTCTCTGGCCCCACCAAGACCACCAAAACCATCTCTGGGCTTGGTGCAG
 GACTCTGAATTCTAACAAATGCCAGTGACTGTGCACTTGAGTTTGAAGGCCAGTGGGCCCTG
 ATGAACGCTCACACCCCTTTCAGCTTAGAGTCTGCATTTGGGCTGTGACGCTTCCACCTGCC
 CAATAGATCTGCTCTGTCTGCGACACCAGATCCACGTGGGGACTCCCTGAGGCCTGCTAAG
 TCCAGGCCCTTGGTCAGGTCAGGTGCACATTGACGGATAAGCCAGGACCGGCACAGAAGTGG
 TTGCCCTTNCATTGCGCCTCCCTGGNCCATGCCCTTCTGGCTTTGGAAAAAATGATGAAGA
 AAACCTTGGCTCCTTCTCTTGTCTGGAAGGGTTACTTGCCTATGGGTTCTGGTGGCTAGAGA
 GAAAAGTAGAAAACAGAGTGCACGTAGGTGTCTAACACAGAGGAGAGTAGGAACAGGGCCGG
 ATACCTGAAGGTACTCCGAGTCCAGCCCCCTGGAGAAGGGGTGCGGGGTGGTGGTAAAGTA
 GCACAACCTACTATTTTTTTTTCTTTTCCATATATTGTTTTTTTAAACACAGAATCTCGTGCT
 GCTGCCCAGGCTGGAGTGCAGTGGCACGATCTGCAAACTCCGCCCTCTGGGTTCAAGTGATT
 CTCTGCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGCACCCACACCTGGCTAATT
 TTTGACTTTTAGTAGAGATGGGGTTTACCATTGTGGCCAGGCTGGCTTTGAACTCTGAC
 CTCAAATGAGCCTCCTGTTCTCAGTCTCCCAAAATGCGCGGATTACAGGATGAGCCACTGTG
 TCTGGCCCTATTTCTTTTAAAAAGTGAAATTAAGAGTTGTTAGTATGCAAACTTGGAAAG
 ATGGAGGAGAAAAAGAAAGGAAGAAAAAATGTACCCATAGTCTCACCAGAGACTATCAT
 TATTTTCGTTTTGTTGACTTCCCTCCACTCTTTTCTTCTTACATAAATTGCGGGTGTTCCT
 TTTACAGCAAAATATCTTTGTATATACAACTTTGTATCTGCTTTTCCACTTATCGTTC
 ATCACTTTATCCAGCACTTCTCTGTGTTTTACAGACCTTTTTTATAAATAAATGTTTCATCA
 GCTGCATAAAAAAAAAAAAAA

0973295-131501

FIGURE 79

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196
<subunit 1 of 1, 332 aa, 1 stop
<MW: 36143, pI: 5.89, NX(S/T): 1
MRLLVLLWGCLLLPGYEALGPPEISGFEGD TVSLQCTYREELRDHRKYWCRKGGILFSRCS
GTIYAEEEGQETMKGRVSI RDSRQELSLIVTLWNLTLDAGEYWC GVEKRGPD ELLISLFV
FPGPCPPSPSPPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQKGTGAEAPPLPG
TSQYGHERTSQYTGTS PHPATSPPPAGSSRPQMQLDSTSAEDTSPALSSGSSKPRVSI PMVRI
LAPVLVLLSLLSAAGLIAFCSHLLLRKEAQQATETQRNEKFWLSRLTAEKEAPSQAPEGD
VISMPPLHTSEEELGFSKFVSA

Important features:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128

[illegible]

TTGTGACTAAAAGCTGTCCTAGCAGGCCAGGGAGTGCAGCTGCAGGCGTGGGGGTGGCAGGA
GCCGCAGAGCCAGAGCAGACAGCCGAGAAACAGGTGGACAGTGTGAAAGAACCAGTGGTCTC
GCTCTGTTGCCAGGCTAGAGTGTACTGGCGTGATCATAGCTACATGCAGCCTCAGACTCCT
GGACTTGAGAAATCCTCCTGCCTTAGCCTCCTGCATATCTGGGACTCCAGGGGTGCACCTCAA
GCCCTGTTTCTTCTCCTTCTGTGAGTGGACACCGGAGGCTGGTGAGCTGCCTGTATCCCAA
AGCTCAGCTCTGAGCCAGAGTGGTGGTGGCTCCACCTCTGCCGCCGCATAGAAGCCAGGAG
CAGGGCTCTCAGAAGCGGGTGGTGCCAGCTGGGATCATGTGTTGTTGGCCCTGGTCTGTCTGC
TCAGCTGCCTGCTACCTCCAGTGAGGCCAAGCTCTACGGTCGTTGTGAACTGGCCAGAGTG
CTACATGACTTCCGGGCTGGACGGATACCGGGGATACAGCCTGGCTGACTGGGTCTGCCTTGC
TTATTTCACAAGCGGTTTCAACGCAGCTGCTTTGGACTACGAGGCTGATGGGAGCACCAACA
ACGGGATCTTCAGATCAACAGCCGGAGGTGGTGAGCAACCTCACCCGAAACGTCCCCAAC
GTGTGCCGGATGTACTGCTCAGATTTGTTGAATCCTAATCTCAAGGATACCGTTATCTGTGC
CATGAAGATAACCCAGAGCCTCAGGCTCTGGGTTACTGGGAGGCCTGGAGGCATCACTGCC
AGGGAAGAAGACATCACTGAATGGGTGGATGGCTGTGACITCTAGATGGACGGAACCATGCA
CAGCAGGCTGGGAAATGTGGTTTGGTTTCCTGACCTAGGCTTGGGAAGACAAGCCAGCGAATA
AAGGATGGTTGAACGTGAAA